#10158

4/12/02

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/889,722A

DATE: 03/27/2002
TIME: 13:32:53

Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\03272002\I889722A.raw

RECEIVED

APR 1 1 2002

TECH CENTER 1600/2900

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 4 <110> APPLICANT: Japan Science and Technology Corporation
 6 <120> TITLE OF INVENTION: Human nucleoprotein having a WW domain and
 7       a polynucleotide encoding the protein
 9 <130> FILE REFERENCE: 09/889,722
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/889,722A
C--> 12 <141> CURRENT FILING DATE: 2001-07-20
14 <150> PRIOR APPLICATION NUMBER: JP11-332572
15 <151> PRIOR FILING DATE: 1999-11-24
17 <160> NUMBER OF SEQ ID NOS: 7
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 704
23 <212> TYPE: PRT
24 <213> ORGANISM: Homo sapiens
26 <400> SEQUENCE: 1
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28   1               5               10              15
29 Ser His Ser Pro Gly Thr Ser Asn Gln Ser Gln Pro Cys Ser Pro Lys
30           20              25              30
31 Pro Ile Arg Leu Val Gln Asp Leu Pro Glu Glu Leu Val His Ala Gly
32           35              40              45
33 Trp Glu Lys Cys Trp Ser Arg Arg Glu Asn Arg Pro Tyr Tyr Phe Asn
34       50              55              60
35 Arg Phe Thr Asn Gln Ser Leu Trp Glu Met Pro Val Leu Gly Gln His
36   65              70              75              80
37 Asp Val Ile Ser Asp Pro Leu Gly Leu Asn Ala Thr Pro Leu Pro Gln
38               85              90              95
39 Asp Ser Ser Leu Val Glu Thr Pro Pro Ala Glu Asn Lys Pro Arg Lys
40           100             105             110
41 Arg Gln Leu Ser Glu Glu Gln Pro Ser Gly Asn Gly Val Lys Lys Pro
42           115             120             125
43 Lys Ile Glu Ile Pro Val Thr Pro Thr Gly Gln Ser Val Pro Ser Ser
44       130             135             140
45 Pro Ser Ile Pro Gly Thr Pro Thr Leu Lys Met Trp Gly Thr Ser Pro
46 145             150             155             160
47 Glu Asp Lys Gln Gln Ala Ala Leu Leu Arg Pro Thr Glu Val Tyr Trp
48               165             170             175
49 Asp Leu Asp Ile Gln Thr Asn Ala Val Ile Lys His Arg Gly Pro Ser
50               180             185             190
51 Glu Val Leu Pro Pro His Pro Glu Val Glu Leu Leu Arg Ser Gln Leu
52           195             200             205
53 Ile Leu Lys Leu Arg Gln His Tyr Arg Glu Leu Cys Gln Gln Arg Glu
54       210             215             220
```

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55 Gly Ile Glu Pro Pro Arg Glu Ser Phe Asn Arg Trp Met Leu Glu Arg
56 225             230             235             240
57 Lys Val Val Asp Lys Gly Ser Asp Pro Leu Leu Pro Ser Asn Cys Glu
58             245             250             255
59 Pro Val Val Ser Pro Ser Met Phe Arg Glu Ile Met Asn Asp Ile Pro
60             260             265             270
61 Ile Arg Leu Ser Arg Ile Lys Phe Arg Glu Glu Ala Lys Arg Leu Leu
62     275             280             285
63 Phe Lys Tyr Ala Glu Ala Ala Arg Arg Leu Ile Glu Ser Arg Ser Ala
64     290             295             300
65 Ser Pro Asp Ser Arg Lys Val Val Lys Trp Asn Val Glu Asp Thr Phe
66 305             310             315             320
67 Ser Trp Leu Arg Lys Asp His Ser Ala Ser Lys Glu Asp Tyr Met Asp
68             325             330             335
69 Arg Leu Glu His Leu Arg Arg Gln Cys Gly Pro His Val Ser Ala Ala
70             340             345             350
71 Ala Lys Asp Ser Val Glu Gly Ile Cys Ser Lys Ile Tyr His Ile Ser
72     355             360             365
73 Leu Glu Tyr Val Lys Arg Ile Arg Glu Lys His Leu Ala Ile Leu Lys
74     370             375             380
75 Glu Asn Asn Ile Ser Glu Glu Val Glu Ala Pro Glu Val Glu Pro Arg
76 385             390             395             400
77 Leu Val Tyr Cys Tyr Pro Val Arg Leu Ala Val Ser Ala Pro Pro Met
78             405             410             415
79 Pro Ser Val Glu Met His Met Glu Asn Asn Val Val Cys Ile Arg Tyr
80             420             425             430
81 Lys Gly Glu Met Val Lys Val Ser Arg Asn Tyr Phe Ser Lys Leu Trp
82             435             440             445
83 Leu Leu Tyr Arg Tyr Ser Cys Ile Asp Asp Ser Ala Phe Glu Arg Phe
84     450             455             460
85 Leu Pro Arg Val Trp Cys Leu Leu Arg Arg Tyr Gln Met Met Phe Gly
86 465             470             475             480
87 Val Gly Leu Tyr Glu Gly Thr Gly Leu Gln Gly Ser Leu Pro Val His
88             485             490             495
89 Val Phe Glu Ala Leu His Arg Leu Phe Gly Val Ser Phe Glu Cys Phe
90             500             505             510
91 Ala Ser Pro Leu Asn Cys Tyr Phe Arg Gln Tyr Cys Ser Ala Phe Pro
92     515             520             525
93 Asp Thr Asp Gly Tyr Phe Gly Ser Arg Gly Pro Cys Leu Asp Phe Ala
94     530             535             540
95 Pro Leu Ser Gly Ser Phe Glu Ala Asn Pro Pro Phe Cys Glu Glu Leu
96 545             550             555             560
97 Met Asp Ala Met Val Ser His Phe Glu Arg Leu Leu Glu Ser Ser Pro
98             565             570             575
99 Glu Pro Leu Ser Phe Ile Val Phe Ile Pro Glu Trp Arg Glu Pro Pro
100             580             585             590
101 Thr Pro Ala Leu Thr Arg Met Glu Gln Ser Arg Phe Lys Arg His Gln
102     595             600             605
103 Leu Ile Leu Pro Ala Phe Glu His Glu Tyr Arg Ser Gly Ser Gln His
```

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```
104      610                615                620
105  Ile Cys Lys Lys Glu Glu Met His Tyr Lys Ala Val His Asn Thr Ala
106  625               630                635                640
107  Val Leu Phe Leu Gln Asn Asp Pro Gly Phe Ala Lys Trp Ala Pro Thr
108               645                650                655
109  Pro Glu Arg Leu Gln Glu Leu Ser Ala Ala Tyr Arg Gln Ser Gly Arg
110               660                665                670
111  Ser His Ser Ser Gly Ser Ser Ser Ser Ser Ser Ser Glu Ala Lys Asp
112          675                680                685
113  Arg Asp Ser Gly Arg Glu Gln Gly Pro Ser Arg Glu Pro His Pro Thr
114          690                695                700
117  <210> SEQ ID NO: 2
118  <211> LENGTH: 2112
119  <212> TYPE: DNA
120  <213> ORGANISM: Homo sapiens
122  <400> SEQUENCE: 2
123  atggccaatg agaatcacgg cagcccccgg gaggaagcgt ccctgctgag tcactcccca   60
124  ggtacctcca atcagagcca gccctgttct ccaaagccaa tccgcctggt tcaggacctc  120
125  ccagaggagc tggtgcatgc aggctgggag aagtgctgga gccggaggga gaatcgtccc  180
126  tactacttca accgattcac caaccagtcc ctgtgggaga tgcccgtgct ggggcagcac  240
127  gatgtgattt cggacccttt ggggctgaat gcgaccccac tgccccaaga ctcaagcttg  300
128  gtggaaactc ccccggctga gaacaagccc agaaagcggc agctctcgga gagcagcca   360
129  agcggcaatg gtgtgaagaa gcccaagatt gaaatcccag tgacacccac aggccagtcg  420
130  gtgcccagct cccccagtat cccaggaacc caacgctga agatgtgggg tacgtcccct  480
131  gaagataaac agcaggcagc tctcctacga cccactgagg tctactggga cctggacatc  540
132  cagaccaatg ctgtcatcaa gcaccggggg ccttcagagg tgctgcccc gcatcccgaa  600
133  gtggaactgc tccgctctca gctcatcctg aagcttcggc agcactatcg ggagctgtgc  660
134  cagcagcgag agggcattga gcctccacgg gagtctttca accgctggat gctggagcgc  720
135  aaggtggtag acaaaggatc tgaccccctg ttgcccagca actgtgaacc agtcgtgtca  780
136  ccttccatgt ttcgtgaaat catgaacgac attcctatca ggttatcccg aatcaagttc  840
137  cgggaggaag ccaagcgcct gctctttaaa tatgcggagg ccgccaggcg gctcatcgag  900
138  tccaggagtg catcccctga cagtaggaag gtggtcaaat ggaatgtgga agacaccttt  960
139  agctggcttc ggaaggacca ctcagcctcc aaggaggact acatggatcg cctggagcat 1020
140  ctgcggaggc agtgtggccc ccacgtctcg gccgcagcca aggactccgt ggaaggcatc 1080
141  tgcagtaaga tctaccacat ctccctggag tacgtcaaac ggatccgaga gaagcacctt 1140
142  gccatcctca aggaaaacaa catctcagag gaggtggagg cccctgaggt ggagccccgc 1200
143  ctagtgtact gctacccagt ccggctggct gtgtctgcac cgcccatgcc cagcgtggag 1260
144  atgcacatgg agaacaacgt ggtctgcatc cggtataagg agagatggt caaggtcagc 1320
145  cgcaactact tcagcaagct gtggctcctt taccgctaca gctgcattga tgactctgcc 1380
146  tttgagaggt tcctgccccg ggtctggtgt cttctccgac ggtaccagat gatgttcggc 1440
147  gtgggcctct acgaggggac tggcctgcag ggatcgctgc ctgtgcatgt ctttgaggcc 1500
148  ctccaccgac tctttggcgt cagcttcgag tgcttcgcct caccccctcaa ctgctacttc 1560
149  cgccagtact gttctgcctt ccccgacaca gacggctact ttggctcccg cgggccctgc 1620
150  ctagactttg ctccactgag tggttcattt gaggccaacc ctcccttctg cgaggagctc 1680
151  atggatgcca tggtctctca ctttgagaga ctgcttgaga gctcaccgga gcccctgtcc 1740
152  ttcatcgtgt catccctga gtggcgggaa cccccaacac cagcgctcac ccgcatggag 1800
153  cagagccgct caaacgcca ccagttgatc ctgcctgcct ttgagcatga gtaccgcagt 1860
154  ggctcccagc acatctgcaa gaaggaggaa atgcactaca aggccgtcca acacggct  1920
155  gtgctcttcc tacagaacga ccctggcttt gccaagtggg cgccgacgcc tgaacggctg 1980
```

```
156 caggagctga gtgctgccta ccggcagtca ggccgcagcc acagctctgg ttcttcctca 2040
157 tcgtcctcct cggaggccaa ggaccgggac tcgggccgtg agcagggtcc tagccgcgag 2100
158 cctcaccccca ct                                                   2112
161 <210> SEQ ID NO: 3
162 <211> LENGTH: 2669
163 <212> TYPE: DNA
164 <213> ORGANISM: Homo sapiens
166 <220> FEATURE:
167 <221> NAME/KEY: CDS
168 <222> LOCATION: (292)..(2406)
170 <400> SEQUENCE: 3
171 acacaagatg gcggcagcgg cgctggggag ggcgaggcgg aggcggcaaa acgggcggtc 60
172 gagcagaacg tgtagccgcg tcccctccag tccgctccgg gcagctgctg atgcaaggaa 120
173 tcccctgggc tcccgtccac tccactgctg accagcccat tcgcctgtgc tgagtcttcc 180
174 tgcaggcctt tccttgcctc tgtgggaccc tgtgggggtc catccggctg gagaagaaaa 240
175 gcctctcatg ctaacgttgc agaccccaga gggtcctgtg tgggtgtgga g atg gcc 297
176                                                         Met Ala
177                                                           1
178 aat gag aat cac ggc agc ccc cgg gag gaa gcg tcc ctg ctg agt cac 345
179 Asn Glu Asn His Gly Ser Pro Arg Glu Glu Ala Ser Leu Leu Ser His
180           5                  10                  15
181 tcc cca ggt acc tcc aat cag agc cag ccc tgt tct cca aag cca atc 393
182 Ser Pro Gly Thr Ser Asn Gln Ser Gln Pro Cys Ser Pro Lys Pro Ile
183          20                  25                  30
184 cgc ctg gtt cag gac ctc cca gag gag ctg gtg cat gca ggc tgg gag 441
185 Arg Leu Val Gln Asp Leu Pro Glu Glu Leu Val His Ala Gly Trp Glu
186  35                  40                  45                  50
187 aag tgc tgg agc cgg agg gag aat cgt ccc tac tac ttc aac cga ttc 489
188 Lys Cys Trp Ser Arg Arg Glu Asn Arg Pro Tyr Tyr Phe Asn Arg Phe
189                  55                  60                  65
190 acc aac cag tcc ctg tgg gag atg ccc gtg ctg ggg cag cac gat gtg 537
191 Thr Asn Gln Ser Leu Trp Glu Met Pro Val Leu Gly Gln His Asp Val
192                  70                  75                  80
193 att tcg gac cct ttg ggg ctg aat gcg acc cca ctg ccc caa gac tca 585
194 Ile Ser Asp Pro Leu Gly Leu Asn Ala Thr Pro Leu Pro Gln Asp Ser
195          85                  90                  95
196 agc ttg gtg gaa act ccc ccg gct gag aac aag ccc aga aag cgg cag 633
197 Ser Leu Val Glu Thr Pro Pro Ala Glu Asn Lys Pro Arg Lys Arg Gln
198         100                 105                 110
199 ctc tcg gaa gag cag cca agc ggc aat ggt gtg aag aag ccc aag att 681
200 Leu Ser Glu Glu Gln Pro Ser Gly Asn Gly Val Lys Lys Pro Lys Ile
201 115                 120                 125                 130
202 gaa atc cca gtg aca ccc aca ggc cag tcg gtg ccc agc tcc ccc agt 729
203 Glu Ile Pro Val Thr Pro Thr Gly Gln Ser Val Pro Ser Ser Pro Ser
204                 135                 140                 145
205 atc cca gga acc cca acg ctg aag atg tgg ggt acg tcc cct gaa gat 777
206 Ile Pro Gly Thr Pro Thr Leu Lys Met Trp Gly Thr Ser Pro Glu Asp
207                 150                 155                 160
208 aaa cag cag gca gct ctc cta cga ccc act gag gtc tac tgg gac ctg 825
```

```
209 Lys Gln Gln Ala Ala Leu Leu Arg Pro Thr Glu Val Tyr Trp Asp Leu
210         165                 170                 175
211 gac atc cag acc aat gct gtc atc aag cac cgg ggg cct tca gag gtg    873
212 Asp Ile Gln Thr Asn Ala Val Ile Lys His Arg Gly Pro Ser Glu Val
213         180                 185                 190
214 ctg ccc ccg cat ccc gaa gtg gaa ctg ctc cgc tct cag ctc atc ctg    921
215 Leu Pro Pro His Pro Glu Val Glu Leu Leu Arg Ser Gln Leu Ile Leu
216 195                 200                 205                 210
217 aag ctt cgg cag cac tat cgg gag ctg tgc cag cag cga gag ggc att    969
218 Lys Leu Arg Gln His Tyr Arg Glu Leu Cys Gln Gln Arg Glu Gly Ile
219                 215                 220                 225
220 gag cct cca cgg gag tct ttc aac cgc tgg atg ctg gag cgc aag gtg   1017
221 Glu Pro Pro Arg Glu Ser Phe Asn Arg Trp Met Leu Glu Arg Lys Val
222                 230                 235                 240
223 gta gac aaa gga tct gac ccc ctg ttg ccc agc aac tgt gaa cca gtc   1065
224 Val Asp Lys Gly Ser Asp Pro Leu Leu Pro Ser Asn Cys Glu Pro Val
225         245                 250                 255
226 gtg tca cct tcc atg ttt cgt gaa atc atg aac gac att cct atc agg   1113
227 Val Ser Pro Ser Met Phe Arg Glu Ile Met Asn Asp Ile Pro Ile Arg
228         260                 265                 ·270
229 tta tcc cga atc aag ttc cgg gag gaa gcc aag cgc ctg ctc ttt aaa   1161
230 Leu Ser Arg Ile Lys Phe Arg Glu Glu Ala Lys Arg Leu Leu Phe Lys
231 275                 280                 285                 290
232 tat gcg gag gcc gcc agg cgg ctc atc gag tcc agg agt gca tcc cct   1209
233 Tyr Ala Glu Ala Ala Arg Arg Leu Ile Glu Ser Arg Ser Ala Ser Pro
234                 295                 300                 305
235 gac agt agg aag gtg gtc aaa tgg aat gtg gaa gac acc ttt agc tgg   1257
236 Asp Ser Arg Lys Val Val Lys Trp Asn Val Glu Asp Thr Phe Ser Trp
237                 310                 315                 320
238 ctt cgg aag gac cac tca gcc tcc aag gag gac tac atg gat cgc ctg   1305
239 Leu Arg Lys Asp His Ser Ala Ser Lys Glu Asp Tyr Met Asp Arg Leu
240                 325                 330                 335
241 gag cat ctg cgg agg cag tgt ggc ccc cac gtc tcg gcc gca gcc aag   1353
242 Glu His Leu Arg Arg Gln Cys Gly Pro His Val Ser Ala Ala Ala Lys
243         340                 345                 350
244 gac tcc gtg gaa ggc atc tgc agt aag atc tac cac atc tcc ctg gag   1401
245 Asp Ser Val Glu Gly Ile Cys Ser Lys Ile Tyr His Ile Ser Leu Glu
246 355                 360                 365                 370
247 tac gtc aaa cgg atc cga gag aag cac ctt gcc atc ctc aag gaa aac   1449
248 Tyr Val Lys Arg Ile Arg Glu Lys His Leu Ala Ile Leu Lys Glu Asn
249                 375                 380                 385
250 aac atc tca gag gag gtg gag gcc cct gag gtg gag ccc cgc cta gtg   1497
251 Asn Ile Ser Glu Glu Val Glu Ala Pro Glu Val Glu Pro Arg Leu Val
252                 390                 395                 400
253 tac tgc tac cca gtc cgg ctg gct gtg tct gca ccg ccc atg ccc agc   1545
254 Tyr Cys Tyr Pro Val Arg Leu Ala Val Ser Ala Pro Pro Met Pro Ser
255                 405                 410                 415
256 gtg gag atg cac atg gag aac aac gtg gtc tgc atc cgg tat aag gga   1593
257 Val Glu Met His Met Glu Asn Asn Val Val Cys Ile Arg Tyr Lys Gly
```

VERIFICATION SUMMARY　　　　　　DATE: 03/27/2002
PATENT APPLICATION: **US/09/889,722A**　　　TIME: 13:32:54

Input Set : **A:\sequence listing.txt**
Output Set: **N:\CRF3\03272002\I889722A.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date